



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/500,018
Source: pc/10
Date Processed by STIC: 8/10/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

~~TO REDUCE ERRORRED SEQUENCE LISTINGS, PLEASE USE THE~~ **CHECKER**
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>16/500,018</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <u> </u> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <u> </u> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <u> </u> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. <u>Do not use tab codes between numbers; use space characters, instead.</u>	
4 <u> </u> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <u> </u> Variable Length	Sequence(s) <u> </u> contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <u> </u> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <u> </u> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <u> </u> Skipped Sequences (OLD RULES)	Sequence(s) <u> </u> missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) <u> </u> SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <u> </u> Skipped Sequences (NEW RULES)	Sequence(s) <u> </u> missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <u> </u> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <u> </u> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <u>✓</u> Use of <220>	Sequence(s) <u>25, 30, 31, 32, 33, 34</u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <u> </u> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <u> </u> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



PCT

*delete
extra <110>;
show <110>
only
once*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/500,018

DATE: 08/10/2004

TIME: 08:26:25

Input Set : A:\PTO.YF.txt

Output Set : N:\CRF4\08102004\J500018.raw

3 <110> APPLICANT: Daiichi Suntory Pharma Co., Ltd.
W--> 4 <110> APPLICANT: Kenji KANGAWA
6 <120> TITLE OF INVENTION: A method for producing a modified peptide
8 <130> FILE REFERENCE: D05F1044
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/500,018
C--> 10 <141> CURRENT FILING DATE: 2004-06-23
10 <150> PRIOR APPLICATION NUMBER: PCT/JP03/04590
11 <151> PRIOR FILING DATE: 2003-04-10
13 <160> NUMBER OF SEQ ID NOS: 39

(global error)

pp 1,3,4,6-11

ERRORED SEQUENCES

15 <210> SEQ ID NO: 1
16 <211> LENGTH: 28
17 <212> TYPE: PRT
18 <213> ORGANISM: Homo sapiens
19 <223> OTHER INFORMATION: Amino acid sequence for human endogenous peptides
of growth hormone

*insert <2207
whenever <221>
<2227, or <2237> is shown. Do not insert any response
to <2207. (header only)*

**Does Not Comply
Corrected Diskette Needed**

20 secretagogue
21 <400> SEQUENCE: 1
22 Gly Ser Ser Phe Leu Ser Pro Glu His Gln Arg Val Gln Gln Arg Lys
23 1 5 10 15
24 Glu Ser Lys Lys Pro Pro Ala Lys Leu Gln Pro Arg
25 20 25
27 <210> SEQ ID NO: 2
28 <211> LENGTH: 27
29 <212> TYPE: PRT
30 <213> ORGANISM: Homo sapiens
31 <223> OTHER INFORMATION: Amino acid sequence for human endogenous peptides
(27 amino acids) of

<2207 insert

32 growth hormone secretagogue
33 <400> SEQUENCE: 2
34 Gly Ser Ser Phe Leu Ser Pro Glu His Gln Arg Val Gln Arg Lys Glu
35 1 5 10 15
36 Ser Lys Lys Pro Pro Ala Lys Leu Gln Pro Arg
37 20 25
39 <210> SEQ ID NO: 3
40 <211> LENGTH: 28
41 <212> TYPE: PRT
42 <213> ORGANISM: Rattus norvegicus
43 <223> OTHER INFORMATION: Amino acid sequence for rat endogenous peptides of
growth hormone
44 secretagogue

<2207 insert

OK-> 45 <400> SEQUENCE: 3

46 Gly Ser Ser Phe Leu Ser Pro Glu His Gln Lys Ala Gln Gln Arg Lys

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/500,018

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\08102004\J500018.raw

47 1 5 10 15

48 Glu Ser Lys Lys Pro Pro Ala Lys Leu Gln Pro Arg

49 20 25

51 <210> SEQ ID NO: 4

52 <211> LENGTH: 27

53 <212> TYPE: PRT

54 <213> ORGANISM: Rattus norvegicus *insert <220>*

55 <223> OTHER INFORMATION: Amino acid sequence for rat endogenous peptides

(27 amino acids) of

56 growth hormone secretagogue

OK 57 <400> SEQUENCE: 4

58 Gly Ser Ser Phe Leu Ser Pro Glu His Gln Lys Ala Gln Arg Lys Glu

59 1 5 10 15

60 Ser Lys Lys Pro Pro Ala Lys Leu Gln Pro Arg

61 20 25

63 <210> SEQ ID NO: 5

64 <211> LENGTH: 28

65 <212> TYPE: PRT

66 <213> ORGANISM: Mus musculus

67 <223> OTHER INFORMATION: Amino acid sequence for mouse endogenous peptides

of growth hormone

68 secretagogue *insert <220>*

OK 69 <400> SEQUENCE: 5

70 Gly Ser Ser Phe Leu Ser Pro Glu His Gln Lys Ala Gln Gln Arg Lys

71 1 5 10 15

72 Glu Ser Lys Lys Pro Pro Ala Lys Leu Gln Pro Arg

73 20 25

75 <210> SEQ ID NO: 6

76 <211> LENGTH: 28

77 <212> TYPE: PRT

78 <213> ORGANISM: Sus scrofa (pig)

79 <223> OTHER INFORMATION: Amino acid sequence for porcine endogenous

peptides of growth hormone

80 secretagogue *insert <220>*

OK 81 <400> SEQUENCE: 6

82 Gly Ser Ser Phe Leu Ser Pro Glu His Gln Lys Val Gln Gln Arg Lys

83 1 5 10 15

84 Glu Ser Lys Lys Pro Ala Ala Lys Leu Lys Pro Arg

85 20 25

87 <210> SEQ ID NO: 7

88 <211> LENGTH: 27

89 <212> TYPE: PRT

90 <213> ORGANISM: Bos taurus

91 <223> OTHER INFORMATION: Amino acid sequence for bovine endogenous peptides

(27 amino acids)

92 of growth hormone secretagogue *insert <220>*

OK 93 <400> SEQUENCE: 7

94 Gly Ser Ser Phe Leu Ser Pro Glu His Gln Lys Leu Gln Arg Lys Glu

95 1 5 10 15

96 Ala Lys Lys Pro Ser Gly Arg Leu Lys Pro Arg

97 20 25

99 <210> SEQ ID NO: 8

100 <211> LENGTH: 27

RAW SEQUENCE LISTING

DATE: 08/10/2004

PATENT APPLICATION: US/10/500,018

TIME: 08:26:26

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\08102004\J500018.raw

101 <212> TYPE: PRT

102 <213> ORGANISM: Ovis aries *insert <2207*103 <223> OTHER INFORMATION: Amino acid sequence for ovine endogenous peptides
(27 amino acids)

104 of growth hormone secretagogue

E--> 105 <400> SEQUENCE: 8

106 Gly Ser Ser Phe Leu Ser Pro Glu His Gln Lys Leu Gln Arg Lys Glu

107 1 5 10 15

108 Pro Lys Lys Pro Ser Gly Arg Leu Lys Pro Arg

109 20 25

111 <210> SEQ ID NO: 9

112 <211> LENGTH: 28

113 <212> TYPE: PRT

114 <213> ORGANISM: Canis familiaris

115 <223> OTHER INFORMATION: Amino acid sequence for dog endogenous peptides
of growth hormone116 secretagogue *insert <2207*

E--> 117 <400> SEQUENCE: 9

118 Gly Ser Ser Phe Leu Ser Pro Glu His Gln Lys Leu Gln Gln Arg Lys

119 1 5 10 15

120 Glu Ser Lys Lys Pro Pro Ala Lys Leu Gln Pro Arg

121 20 25

168 <210> SEQ ID NO: 13

169 <211> LENGTH: 24

170 <212> TYPE: PRT

171 <213> ORGANISM: Gallus domesticus

172 <223> OTHER INFORMATION: Amino acid sequence for chicken endogenous
peptides of growth hormone173 secretagogue *insert <2207*

E--> 174 <400> SEQUENCE: 13

175 Gly Ser Ser Phe Leu Ser Pro Thr Tyr Lys Asn Ile Gln Gln Gln Lys

176 1 5 10 15

177 Gly Thr Arg Lys Pro Thr Ala Arg

178 20

180 <210> SEQ ID NO: 14

181 <211> LENGTH: 24

182 <212> TYPE: PRT

183 <213> ORGANISM: Gallus domesticus

184 <223> OTHER INFORMATION: Amino acid sequence for chicken endogenous
peptides of growth hormone185 secretagogue *insert <2207*

E--> 186 <400> SEQUENCE: 14

187 Gly Ser Ser Phe Leu Ser Pro Thr Tyr Lys Asn Ile Gln Gln Gln Lys

188 1 5 10 15

189 Asp Thr Arg Lys Pro Thr Ala Arg

190 20

192 <210> SEQ ID NO: 15

193 <211> LENGTH: 26

194 <212> TYPE: PRT

195 <213> ORGANISM: Gallus domesticus

196 <223> OTHER INFORMATION: Amino acid sequence for chicken endogenous
peptides of growth hormone197 secretagogue *insert <2207*

OK
E--> 198 <400> SEQUENCE: 15

RAW SEQUENCE LISTING

DATE: 08/10/2004

PATENT APPLICATION: US/10/500,018

TIME: 08:26:26

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\08102004\J500018.raw

199 Gly Ser Ser Phe Leu Ser Pro Thr Tyr Lys Asn Ile Gln Gln Gln Lys
 200 1 5 10 15
 201 Asp Thr Arg Lys Pro Thr Ala Arg Leu His
 202 20 25
 204 <210> SEQ ID NO: 16
 205 <211> LENGTH: 27
 206 <212> TYPE: PRT
 207 <213> ORGANISM: Rana cafesbeiana
 208 <223> OTHER INFORMATION: Amino acid sequence for frog endogenous peptides
 of growth hormone
 209 secretagogue *insert 2207*
 E--> 210 <400> SEQUENCE: 16
 211 Gly Leu Thr Phe Leu Ser Pro Ala Asp Met Gln Lys Ile Ala Glu Arg
 212 1 5 10 15
 213 Gln Ser Gln Asn Lys Leu Arg His Gly Asn Met
 214 20 25
 216 <210> SEQ ID NO: 17
 217 <211> LENGTH: 28
 218 <212> TYPE: PRT
 219 <213> ORGANISM: Rana cafesbeiana
 220 <223> OTHER INFORMATION: Amino acid sequence for frog endogenous peptides
 of growth hormone
 221 secretagogue *insert 2207*
 E--> 222 <400> SEQUENCE: 17
 223 Gly Leu Thr Phe Leu Ser Pro Ala Asp Met Gln Lys Ile Ala Glu Arg
 224 1 5 10 15
 225 Gln Ser Gln Asn Lys Leu Arg His Gly Asn Met Asn
 226 20 25
 258 <210> SEQ ID NO: 20
 259 <211> LENGTH: 23
 260 <212> TYPE: PRT
 261 <213> ORGANISM: Silurus asotus
 262 <223> OTHER INFORMATION: Amino acid sequence for catfish endogenous
 peptides of growth hormone
 263 secretagogue *insert 2207*
 E--> 264 <400> SEQUENCE: 20
 265 Gly Ser Ser Phe Leu Ser Pro Thr Gln Lys Pro Gln Asn Arg Gly Asp
 266 1 5 10 15
 267 Arg Lys Pro Pro Arg Val Gly
 268 20
 270 <210> SEQ ID NO: 21
 271 <211> LENGTH: 28
 272 <212> TYPE: PRT
 273 <213> ORGANISM: Equus caballus
 274 <223> OTHER INFORMATION: Amino acid sequence for equine endogenous
 peptides of growth hormone
 275 secretagogue *insert 2207*
 E--> 276 <400> SEQUENCE: 21
 277 Gly Ser Ser Phe Leu Ser Pro Glu His His Lys Val Gln His Arg Lys
 278 1 5 10 15
 279 Glu Ser Lys Lys Pro Pro Ala Lys Leu Lys Pro Arg
 280 20 25
 456 <210> SEQ ID NO: 39

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/500,018

DATE: 08/10/2004

TIME: 08:26:26

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\08102004\J500018.raw

457 <211> LENGTH: 44
458 <212> TYPE: DNA
459 <213> ORGANISM: Artificial sequence
@k> 460 <220> FEATURE:
461 <223> OTHER INFORMATION: GR2r
W--> 462 <400> SEQUENCE: 39
463 tcgactcatc gtggctgcag tttagctggc ttcttggatt cctt 44
E--> 464 1/16

delete

give source of genetic material (see item 11 on Error Summary Sheet)

Please check other sequences with a <213> Artificial Sequence

response, to ensure the <223> response gives source of genetic material.

see pages 8-11 for more errors

<210> 23

<211> 4

<212> PRT

<213> Artificial sequence

what about the source of the 4 amino acids?

<220>

<223> Amino acid sequence adjacent to a site cleaved by blood coagulation

Factor Xa

<400> 23

Ile Glu Gly Arg

1

<210> 24

<211> 7

<212> PRT

<213> Artificial sequence

what is the source of the genetic material in the 7 amino acids?

<220>

<223> Amino acid sequence containing a site cleaved by renin

<400> 24

Pro Phe His Leu Leu Val Tyr

1

5

<210> 25

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> ← explanation goes on this line. See item 11 on Euro summary sheet

<400> 25

35

<210> 28

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> primer ORI-RR

<400> 28

ggttccggat ccccttctcg acatgccgg gaacac

36

<210> 29

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> primer SAL*R

<400> 29

ataagtcgac ttatcgtggc tgcag

25

<210> 30

<211> 13

<212> PRT

<213> Artificial sequence

<220>

<223> ← Explanation needed here

<400> 30

Arg His His Gly Ser Gly Ser Pro Ser Arg His Arg Arg

1

5

10

<210> 31

<211> 13

<212> PRT

<213> Artificial sequence

<220>

<223> ← *que exploration*

<400> 31

Arg His His Gly Ser Gly Ser Pro Ser Arg His Pro Arg

1

5

10

<210> 32

<211> 13

<212> PRT

<213> Artificial sequence

<220>

<223> ← *que exploration*

<400> 32

Arg His His Gly Ser Gly Ser Pro Ser Arg His Lys Arg

1

5

10

<210> 33

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> ← *que exploration*

<400> 33

Gly Ser Ser Phe Leu Ser Pro

10/500, 11

1

5

<210> 34

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> ← give explanation

<400> 34

Phe Leu Ser Pro

1

<210> 35

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> linker sequence

<400> 35

Arg Arg His His Gly Ser Gly Ser Pro Ser Arg His Pro Arg

1

5

10

<210> 36

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> h8-28f1

<400> 36

← explain source of genetic material

FYI: do not insert page numbers in computer readable form of Sequence Listings (per Sequence Rules)

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/500,018

DATE: 08/10/2004

TIME: 08:26:27

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\08102004\J500018.raw

L:4 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:21 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:1
L:21 M:283 W: Missing Blank Line separator, <400> field identifier
L:33 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:2
L:33 M:283 W: Missing Blank Line separator, <400> field identifier
L:45 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:3
L:45 M:283 W: Missing Blank Line separator, <400> field identifier
L:57 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:4
L:57 M:283 W: Missing Blank Line separator, <400> field identifier
L:69 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:5
L:69 M:283 W: Missing Blank Line separator, <400> field identifier
L:81 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:6
L:81 M:283 W: Missing Blank Line separator, <400> field identifier
L:93 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:7
L:93 M:283 W: Missing Blank Line separator, <400> field identifier
L:105 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:8
L:105 M:283 W: Missing Blank Line separator, <400> field identifier
L:117 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:9
L:117 M:283 W: Missing Blank Line separator, <400> field identifier
L:127 M:283 W: Missing Blank Line separator, <220> field identifier
L:132 M:283 W: Missing Blank Line separator, <400> field identifier
L:142 M:283 W: Missing Blank Line separator, <220> field identifier
L:147 M:283 W: Missing Blank Line separator, <400> field identifier
L:157 M:283 W: Missing Blank Line separator, <220> field identifier
L:162 M:283 W: Missing Blank Line separator, <400> field identifier
L:174 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:13
L:174 M:283 W: Missing Blank Line separator, <400> field identifier
L:186 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:14
L:186 M:283 W: Missing Blank Line separator, <400> field identifier
L:198 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:15
L:198 M:283 W: Missing Blank Line separator, <400> field identifier
L:210 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:16
L:210 M:283 W: Missing Blank Line separator, <400> field identifier
L:222 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:17
L:222 M:283 W: Missing Blank Line separator, <400> field identifier
L:232 M:283 W: Missing Blank Line separator, <220> field identifier
L:237 M:283 W: Missing Blank Line separator, <400> field identifier
L:247 M:283 W: Missing Blank Line separator, <220> field identifier
L:252 M:283 W: Missing Blank Line separator, <400> field identifier
L:264 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:20
L:264 M:283 W: Missing Blank Line separator, <400> field identifier
L:276 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:21
L:276 M:283 W: Missing Blank Line separator, <400> field identifier
L:286 M:283 W: Missing Blank Line separator, <220> field identifier
L:288 M:283 W: Missing Blank Line separator, <400> field identifier
L:296 M:283 W: Missing Blank Line separator, <220> field identifier

VERIFICATION SUMMARY

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\08102004\J500018.raw

L:299 M:283 W: Missing Blank Line separator, <400> field identifier
 L:307 M:283 W: Missing Blank Line separator, <220> field identifier
 L:309 M:283 W: Missing Blank Line separator, <400> field identifier
 L:317 M:283 W: Missing Blank Line separator, <220> field identifier
 L:319 M:283 W: Missing Blank Line separator, <400> field identifier
 L:319 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:318
 L:327 M:283 W: Missing Blank Line separator, <220> field identifier
 L:329 M:283 W: Missing Blank Line separator, <400> field identifier
 L:341 M:283 W: Missing Blank Line separator, <220> field identifier
 L:343 M:283 W: Missing Blank Line separator, <400> field identifier
 L:355 M:283 W: Missing Blank Line separator, <220> field identifier
 L:357 M:283 W: Missing Blank Line separator, <400> field identifier
 L:364 M:283 W: Missing Blank Line separator, <220> field identifier
 L:366 M:283 W: Missing Blank Line separator, <400> field identifier
 L:373 M:283 W: Missing Blank Line separator, <220> field identifier
 L:375 M:283 W: Missing Blank Line separator, <400> field identifier
 L:375 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:30,Line#:374
 L:383 M:283 W: Missing Blank Line separator, <220> field identifier
 L:385 M:283 W: Missing Blank Line separator, <400> field identifier
 L:385 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:31,Line#:384
 L:393 M:283 W: Missing Blank Line separator, <220> field identifier
 L:395 M:283 W: Missing Blank Line separator, <400> field identifier
 L:395 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:32,Line#:394
 L:403 M:283 W: Missing Blank Line separator, <220> field identifier
 L:405 M:283 W: Missing Blank Line separator, <400> field identifier
 L:405 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:33,Line#:404
 L:413 M:283 W: Missing Blank Line separator, <220> field identifier
 L:415 M:283 W: Missing Blank Line separator, <400> field identifier
 L:415 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:34,Line#:414
 L:423 M:283 W: Missing Blank Line separator, <220> field identifier
 L:425 M:283 W: Missing Blank Line separator, <400> field identifier
 L:433 M:283 W: Missing Blank Line separator, <220> field identifier
 L:435 M:283 W: Missing Blank Line separator, <400> field identifier
 L:442 M:283 W: Missing Blank Line separator, <220> field identifier
 L:444 M:283 W: Missing Blank Line separator, <400> field identifier
 L:451 M:283 W: Missing Blank Line separator, <220> field identifier
 L:453 M:283 W: Missing Blank Line separator, <400> field identifier
 L:460 M:283 W: Missing Blank Line separator, <220> field identifier
 L:462 M:283 W: Missing Blank Line separator, <400> field identifier
 L:466 M:254 E: No. of Bases conflict, LENGTH:Input:16 Counted:45 SEQ:39
 L:466 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:466 M:252 E: No. of Seq. differs, <211> LENGTH:Input:44 Found:45 SEQ:39